

SEQUENCE LISTING

<110> Julius, David J.
Caterina, Michael J.
Brake, Anthony J.

<120> Nucleic acid sequences encoding
capsaicin receptor and capsaicin receptor-related
polypeptides and uses thereof

<130> UCAL084CON

<140> Unassigned

<141> 2001-10-15

<150> 09/235,451

<151> 1999-01-22

<150> 60/072,151

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<150> 08/915,461

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<160> 48

<170> FastSEQ for Windows Version 4.0

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<213> R. rattus

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625				630				635				640				
Leu	Ile	Ala	Leu	Met	Ser	Glu	Thr	Val	Asn	His	Val	Ala	Asp	Asn	Ser	
				645					650					655		
Trp	Ser	Ile	Trp	Lys	Leu	Gln	Lys	Ala	Ile	Ser	Val	Leu	Glu	Met	Glu	
				660					665					670		
Asn	Gly	Tyr	Trp	Trp	Cys	Arg	Arg	Lys	Lys	His	Arg	Glu	Gly	Arg	Leu	
				675					680					685		
Leu	Lys	Val	Gly	Thr	Arg	Gly	Asp	Gly	Thr	Pro	Asp	Glu	Arg	Trp	Cys	
				690					695					700		
Phe	Arg	Val	Glu	Glu	Val	Asn	Trp	Ala	Ala	Trp	Glu	Lys	Thr	Leu	Pro	
705				710				715				720				
Thr	Leu	Ser	Glu	Asp	Pro	Ser	Gly	Pro	Gly	Ile	Thr	Gly	Asn	Lys	Lys	
				725					730					735		
Asn	Pro	Thr	Ser	Lys	Pro	Gly	Lys	Asn	Ser	Ala	Ser	Glu	Glu	Asp	His	
				740					745					750		
Leu	Pro	Leu	Gln	Val	Leu	Gln	Ser	Pro								
				755					760							

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<210> 5
<211> 273
<212> DNA
<213> Homo sapiens
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5070250

<220>
 <221> misc_feature
 <222> (1)...(273)
 <223> n = A,T,C or G

<400> 5
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 accagcaagt acctcaccga ctccgaatac acagagggct ncnacaggta agacgtgcct 120
 gatgaaggct gtgctgaacc ttaaggacgg ggtcaatgcc tgcattctgc cactgctgca 180
 gatcgachgg gactctggca atcctcagcc cctggtaaata gccagtgca cagatgacta 240
 ttaccgaggc cacagcnctc tgcacatcgc cat 273

<210> 6
 <211> 768
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(768)
 <223> n = A,T,C or G

<400> 6
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 tcctggagaa cccacaccag cccgccagcc tgcagnncac tgactcccag ggcaacacag 120
 tcctgcatgc cctagtgtatg atctcggaca actcagctga gaacattgca ctggtgacca 180
 gcatgtatga tgggctcctc caagctgggg cccgncctct gccctaccgt gcnagcttga 240
 ggacatccgc aacctgcagg atctcacgcc tctgnaannt ggccgccaag gagggcaaga 300
 tcgrrwtty maggcacatc ctnnsmagcg ggrrktttca ggactgnagc cacctttnc 360
 ccgaaaagttc accgagtggg ngctannkcg gcctgtccgg gntgtcgtg tnatgacctg 420
 gnyttctnt ggacagctgt naggagaact cagtgtcgtg gatcattgcc tttcattngc 480
 aaragcccg accgacaccg aatggctcgtt ttggagcccc tgaacaaact gctgcaggcn 540
 gaaatgggat ctgctcatcc ccaagttctt cttaaaactc ctgtgtaatc tgatntacat 600
 gttcatcttc amckctgttg cctaccatca gcctaccng aagaagcagg ccgccccctca 660
 cctgaaagcg gaggttgga actccatgct gctgacgggc cacatcctta tcctgctagg 720
 ggggatctac ctctcgtgg ggcaaaagt gaaattttgg gggggaat 768

<210> 7
 <211> 650
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(650)
 <223> n = A,T,C or G

<400> 7
 tgtttcctgg ccacagagtg gtacctgcc ctgcttgtgt ctgcgctggt gctgggctgg 60
 ctgaacctgc ttactatac acgtggcttc cagcacacag gcactctacag tgtcatgac 120
 cagaagccct ggtgagcctg agccaggatt ggcgccccga agctcctaca ggccccaatg 180

<222> (1)...(471)
<223> n = A,T,C or G

<400> 10
cctgcagaag agcancangc gectgannga cagcgagttc aaagacccag agacgggaaa 60
gacctgtctg ctcaaagcca tgetcaatct gcacaatggg cagaacgaca ccattgtctt 120
gctcctggac attgcccggg agacagatag cctgaagcag tttgtcaatg ccagctacac 180
agacagctac tacaagggcc agacagcatt acacattgcc attgaaaggc ggaacatggc 240
nctggtgacc ctcttgggtg agaatggagc agatgtccag gctgctgctg acggggactt 300
cttcnanaaa accaanggga ggccctggctt ctactttggg gagctgcccc tgtccctggc 360
tgcgtgcacc aaccagctgg ccattgtgaa attcctgctg cagaactcct gggcagcctg 420
cagacatcag tggcncggga ttcngtgggc aacacngtgc tgcacnccct t 471

<210> 11
<211> 450
<212> DNA
<213> M. musculus

<400> 11
caagtgtcgg ggatctgcct tgcagggcca agttaattct ttacaacagc ctgtattcca 60
catgtctgga gctgttcaag ttcaccatcg gcatgggtga cctggagttc accgagaact 120
atgacttcaa ggctgtcttt catcatcctg ttactggcct atgtgattct cacctacatc 180
ctcctgctca acatgctcat tgetctcatg ggcgagactg tcaacaagat tgcacaagag 240
agcaagaaca tctggaagct gcagcgagcc atcaccatcc tggatacaga gaagagtttc 300
ctgaagtgca tgaggaaggc cttccgctcc ggcaagctgc tgcaggtggg gttcacgccg 360
gacggcaagg atgacttccg gtgggtgcttc aggggtggatg aggtgaactg gactacctgg 420
aacaccaacg tgggcatcat caacgaggac 450

<210> 12
<211> 18
<212> DNA
<213> R. rattus

<400> 12
gaccagcaag tacctcac 18

<210> 13
<211> 49
<212> DNA
<213> R. rattus

<400> 13
ctcccatgca gccagttta cttcctccac cctgaagcac cagcgctca 49

<210> 14
<211> 71
<212> PRT
<213> R. rattus

<400> 14
Glu Leu Phe Lys Phe Thr Ile Gly Met Gly Asp Leu Glu Phe Thr Glu

405101 6063/66

```

          20          25          30
Gly Ser Tyr Ser Val Ile Asn Ile Ile Val Leu Leu Asn Met Leu Ile
          35          40          45
Ala Met Met Ser Asn Ser Tyr Gln Ile Ile Ser Glu Arg Ala Asp Val
          50          55          60
Glu Trp Lys Phe Ala Arg Ser Gln Leu Trp Met
65          70          75

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<210> 18
 <211> 75
 <212> PRT
 <213> B. taurus

```

<400> 18
Ser Leu Phe Trp Ser Ile Phe Gly Leu Ile Asn Leu Tyr Val Thr Asn
 1          5          10          15
Val Lys Ala Gln His Glu Phe Thr Glu Phe Val Gly Ala Thr Met Phe
          20          25          30
Gly Thr Tyr Asn Val Ile Ser Leu Val Val Leu Leu Asn Met Leu Ile
          35          40          45
Ala Met Met Asn Asn Ser Tyr Gln Leu Ile Ala Asp His Ala Asp Ile
          50          55          60
Glu Trp Lys Phe Ala Arg Thr Lys Leu Trp Met
65          70          75

```

<210> 19
 <211> 61
 <212> PRT
 <213> C. elegans

```

<400> 19
Arg Thr Phe Ile Met Thr Ile Gly Glu Phe Ser Val Leu Tyr Arg Glu
 1          5          10          15
Met Ser Ala Cys Asp Asn Phe Trp Met Lys Trp Ile Gly Lys Leu Ile
          20          25          30
Phe Val Ile Phe Glu Thr Phe Val Ser Ile Leu Gln Phe Asn Leu Leu
          35          40          45
Ile Ala Met Met Thr Arg Thr Tyr Glu Thr Ile Phe Leu
          50          55          60

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<210> 20
 <211> 350
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(350)
 <223> n = A,T,C or G

<400> 20

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tccagttttc	aggttggaga	cattagatgg	aggccaagaa	gatggctctg	aggcggacag	120
aggaaagctg	gattttggga	gcgggctgcc	tcccatggag	tcacagttcc	agggcgagga	180
ccggaatttc	gcccctcaga	taagagtcaa	cctcaactac	cgaaagggaa	caggtgccag	240
tcagccggat	ccaaaccgat	ttgaccgaga	tcggtctctc	aatgcggtct	cccggggtgt	300
ccccgaggat	ctggctggac	ttccagagta	cctgagcaag	accagcaagt		350

<210> 21
 <211> 764
 <212> DNA
 <213> Homo sapiens

<400> 21						
tcggtgagct	accctctctc	ttggccgctt	gcaccaagca	gtgggatgtg	gtaagctacc	60
tcctggagaa	cccacaccag	cccgccagcc	tgcaggccac	tgactcccag	ggcaacacag	120
tcctgcatgc	cctagtgatg	atctcggaca	actcagctga	gaacattgca	ctggtgacca	180
gcatgtatga	tgggctctc	caagctgggg	ccgcctctg	ccctaccgtg	cagcttgagg	240
acatccgcaa	cctgcaggat	ctcacgcctc	tgaagctggc	cgccaaggag	ggcaagatcg	300
rratyttcaa	ggcacatcct	tgcaagcggg	aagttttcag	gactgaagcc	accttttccc	360
cgaaagttca	ccgagtgggtg	gctaattggg	cctgtccggg	ttgtcgtgtg	aatgacctgg	420
gctttctgtg	gacagctgtg	aggagaactc	agtgtcgrrr	atcattgcct	ttcatttgca	480
aragcccgc	cgacaccgaa	tggtcgtttt	ggagcccctg	aacaaactgc	tgcaaggcga	540
atgggatctg	ctcatcccca	agttcttctt	aaacttcctg	tgtaatctga	ttacatgttc	600
atcttcaccg	ctgttgctta	ccatcagcct	accctgaaga	agcaggccgc	ccctcacctg	660
aaagcggagg	ttggaaactc	catgctgctg	acgggccaca	tccttatcct	gctagggggg	720
atctacctcc	tcgtggggca	aaagtggaaa	ttttgggggg	gaat		764

<210> 22
 <211> 884
 <212> DNA
 <213> Homo sapiens

<400> 22						
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cagaagccct	ggtgagcctg	agccaggatt	ggcgccccga	agctcctaca	ggccccaatg	180
ccacagagtc	agtgcagccc	atggagggac	aggaggacga	gggcaacggg	gcccagtaca	240
ggggatctct	ggwagcctcc	ttggagctct	tcaaattcac	catcggcata	ggcagctggg	300
ccttcacagga	gcagctgcac	ttccgcggca	tgggtgctgt	gctgctgctg	gcctacgtgc	360
tgctcaccta	catcctgctg	ctcaacatgc	tcatcgccct	cwtgagcgag	accgtcaaca	420
gtgtcgccac	tgacagctgg	agcatctgga	agctgcagaa	agccatctct	gtcctggaga	480
tggagaatgg	ctattgggtg	tgcaaggaaga	agcagcgggc	aggtgtgatg	ctgaccgttg	540
gcactaagcc	agatggcagc	ccsgatgagc	gctggtgctt	caggggtggag	gaggtgaact	600
gggcttcatg	ggagcagacg	ctgcctacgc	tgtgtgagga	cccgtcaggg	gcaggtgtcc	660
ctcgaactct	cgagaaccct	gtcctggctt	ccccctccaa	ggaggatgag	gatgggtgct	720
ctgaggaaaa	ctatgtgccc	gtccagctcc	tccagtccaa	ctgatggccc	agatgcagca	780
ggaggccaga	ggacagagca	gaggatcttt	ccaaccacat	ctgctggctc	tggggtccca	840
gtgaattctg	gtggcaaata	tatatatttc	ctaammwmaa	aaac		884

<210> 23
 <211> 727

<212> PRT
 <213> Homo sapiens

<220>
 <221> VARIANT
 <222> (1)...(727)
 <223> Xaa = Any Amino Acid

<400> 23

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          20          25          30
Gly Ser Gly Leu Pro Pro Met Glu Ser Gln Phe Gln Gly Glu Asp Arg
          35          40          45
Lys Phe Ala Pro Gln Ile Arg Val Asn Leu Asn Tyr Arg Lys Gly Thr
          50          55          60
Gly Ala Ser Gln Pro Asp Pro Asn Arg Phe Asp Arg Asp Arg Leu Phe
65          70          75          80
Asn Ala Val Ser Arg Gly Val Pro Glu Asp Leu Ala Gly Leu Pro Glu
          85          90          95
Tyr Leu Ser Lys Thr Ser Lys Tyr Leu Thr Asp Ser Glu Tyr Thr Glu
          100          105          110
Gly Ser Thr Gly Lys Thr Cys Leu Met Lys Ala Val Leu Asn Leu Lys
          115          120          125
Asp Gly Val Asn Ala Cys Ile Leu Pro Leu Leu Gln Ile Asp Arg Asp
          130          135          140
Ser Gly Asn Pro Gln Pro Leu Val Asn Ala Gln Cys Thr Asp Asp Tyr
          145          150          155          160
Tyr Arg Gly His Ser Ala Leu His Ile Ala Ile Glu Lys Arg Ser Leu
          165          170          175
Gln Cys Val Lys Leu Leu Val Glu Asn Gly Ala Asn Val His Ala Arg
          180          185          190
Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
          195          200          205
Gly Glu Leu Pro Leu Ser Leu Ala Ala Cys Thr Lys Gln Trp Asp Val
          210          215          220
Val Ser Tyr Leu Leu Glu Asn Pro His Gln Pro Ala Ser Leu Gln Ala
          225          230          235          240
Thr Asp Ser Gln Gly Asn Thr Val Leu His Ala Leu Val Met Ile Ser
          245          250          255
Asp Asn Ser Ala Glu Asn Ile Ala Leu Val Thr Ser Met Tyr Asp Gly
          260          265          270
Leu Leu Gln Ala Gly Ala Arg Leu Cys Pro Thr Val Gln Leu Glu Asp
          275          280          285
Ile Arg Asn Leu Gln Asp Leu Thr Pro Leu Lys Leu Ala Ala Lys Glu
          290          295          300
Gly Lys Ile Xaa Ile Phe Xaa Arg His Ile Leu Ala Ser Gly Lys Phe
          305          310          315          320
Ser Gly Leu Lys Pro Pro Phe Pro Arg Lys Phe Thr Glu Trp Trp Leu
          325          330          335

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097636-4154

Met Gly Pro Val Arg Val Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 340 345 350
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 355 360 365
 Pro Asp Arg His Arg Met Val Val Leu Glu Pro Leu Asn Lys Leu Leu
 370 375 380
 Gln Ala Lys Trp Asp Leu Leu Ile Pro Lys Phe Phe Leu Asn Phe Leu
 385 390 395 400
 Cys Asn Leu Xaa Tyr Met Phe Ile Phe Thr Ala Val Ala Tyr His Gln
 405 410 415
 Pro Thr Leu Lys Lys Gln Ala Ala Pro His Leu Lys Ala Glu Val Gly
 420 425 430
 Asn Ser Met Leu Leu Thr Gly His Ile Leu Ile Leu Leu Gly Gly Ile
 435 440 445
 Tyr Leu Leu Val Gly Gln Lys Trp Lys Phe Trp Xaa Xaa Xaa Xaa Xaa
 450 455 460
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe Pro Gly His Arg Val
 465 470 475 480
 Val Pro Ala Pro Ala Cys Val Cys Ala Gly Ala Gly Leu Ala Glu Pro
 485 490 495
 Ala Leu Leu Tyr Thr Trp Leu Pro Ala His Arg His Leu Gln Cys His
 500 505 510
 Asp Pro Glu Ala Leu Val Ser Leu Ser Gln Asp Trp Arg Pro Glu Ala
 515 520 525
 Pro Thr Gly Pro Asn Ala Thr Glu Ser Val Gln Pro Met Glu Gly Gln
 530 535 540
 Glu Asp Glu Gly Asn Gly Ala Gln Tyr Arg Gly Ile Leu Xaa Ala Ser
 545 550 555 560
 Leu Glu Leu Phe Lys Phe Thr Ile Gly Met Gly Glu Leu Ala Phe Gln
 565 570 575
 Glu Gln Leu His Phe Arg Gly Met Val Leu Leu Leu Leu Leu Ala Tyr
 580 585 590
 Val Leu Leu Thr Tyr Ile Leu Leu Leu Asn Met Leu Ile Ala Leu Xaa
 595 600 605
 Ser Glu Thr Val Asn Ser Val Ala Thr Asp Ser Trp Ser Ile Trp Lys
 610 615 620
 Leu Gln Lys Ala Ile Ser Val Leu Glu Met Glu Asn Gly Tyr Trp Trp
 625 630 635 640
 Cys Arg Lys Lys Gln Arg Ala Gly Val Met Leu Thr Val Gly Thr Lys
 645 650 655
 Pro Asp Gly Ser Pro Asp Glu Arg Trp Cys Phe Arg Val Glu Glu Val
 660 665 670
 Asn Trp Ala Ser Trp Glu Gln Thr Leu Pro Thr Leu Cys Glu Asp Pro
 675 680 685
 Ser Gly Ala Gly Val Pro Arg Thr Leu Glu Asn Pro Val Leu Ala Ser
 690 695 700
 Pro Pro Lys Glu Asp Glu Asp Gly Ala Ser Glu Glu Asn Tyr Val Pro
 705 710 715 720
 Val Gln Leu Leu Gln Ser Asn
 725

SECRET

16

caaggaggac aattaaaacg cttccttcat aagagcgggg atttatggaa aaaggccaaa
gaagctagga aatgactgtg tgcaaggatt cattaagtat cttgaataaa ctacttgttg
tttaaaaaaa aaaaaaaaaa aaaaa

2760
2820
2845

<210> 25
<211> 843
<212> PRT
<213> chicken

<400> 25
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Leu Glu Thr Ala Asp Asn Leu Gln Gly Thr Phe Ser Asn Lys Val Gln
35 40 45
Pro Ser Lys Ser Asn Ile Phe Ala Arg Arg Gly Arg Phe Val Met Gly
50 55 60
Asp Cys Asp Lys Asp Met Ala Pro Met Asp Ser Phe Tyr Gln Met Asp
65 70 75 80
His Leu Met Ala Pro Ser Val Ile Lys Phe His Ala Asn Met Glu Arg
85 90 95
Gly Lys Leu His Lys Leu Leu Ser Thr Asp Ser Ile Thr Gly Cys Ser
100 105 110
Glu Lys Ala Phe Lys Phe Tyr Asp Arg Arg Arg Ile Phe Asp Ala Val
115 120 125
Ala Arg Gly Ser Thr Lys Asp Leu Asp Asp Leu Leu Leu Tyr Leu Asn
130 135 140
Arg Thr Leu Lys His Leu Thr Asp Asp Glu Phe Lys Glu Pro Glu Thr
145 150 155 160
Gly Lys Thr Cys Leu Leu Lys Ala Met Leu Asn Leu His Asp Gly Lys
165 170 175
Asn Asp Thr Ile Pro Leu Leu Leu Asp Ile Ala Lys Lys Thr Gly Thr
180 185 190
Leu Lys Glu Phe Val Asn Ala Glu Tyr Thr Asp Asn Tyr Tyr Lys Gly
195 200 205
Gln Thr Ala Leu His Ile Ala Ile Glu Arg Arg Asn Met Tyr Leu Val
210 215 220
Lys Leu Leu Val Gln Asn Gly Ala Asp Val His Ala Arg Ala Cys Gly
225 230 235 240
Glu Phe Phe Arg Lys Ile Lys Gly Lys Pro Gly Phe Tyr Phe Gly Glu
245 250 255
Leu Pro Leu Ser Leu Ala Ala Cys Thr Asn Gln Leu Cys Ile Val Lys
260 265 270
Phe Leu Leu Glu Asn Pro Tyr Gln Ala Ala Asp Ile Ala Ala Glu Asp
275 280 285
Ser Met Gly Asn Met Val Leu His Thr Leu Val Glu Ile Ala Asp Asn
290 295 300
Thr Lys Asp Asn Thr Lys Phe Val Thr Lys Met Tyr Asn Asn Ile Leu
305 310 315 320
Ile Leu Gly Ala Lys Ile Asn Pro Ile Leu Lys Leu Glu Glu Leu Thr

				325						330						335							
Asn	Lys	Lys	Gly	Leu	Thr	Pro	Leu	Thr	Leu	Ala	Ala	Lys	Thr	Gly	Lys								
			340						345						350								
Ile	Gly	Ile	Phe	Ala	Tyr	Ile	Leu	Arg	Arg	Glu	Ile	Lys	Asp	Pro	Glu								
		355						360						365									
Cys	Arg	His	Leu	Ser	Arg	Lys	Phe	Thr	Glu	Trp	Ala	Tyr	Gly	Pro	Val								
	370						375						380										
His	Ser	Ser	Leu	Tyr	Asp	Leu	Ser	Cys	Ile	Asp	Thr	Cys	Glu	Lys	Asn								
385						390						395						400					
Ser	Val	Leu	Glu	Ile	Ile	Ala	Tyr	Ser	Ser	Glu	Thr	Pro	Asn	Arg	His								
		405						410						415									
Glu	Met	Leu	Leu	Val	Glu	Pro	Leu	Asn	Arg	Leu	Leu	Gln	Asp	Lys	Trp								
		420						425						430									
Asp	Arg	Phe	Val	Lys	His	Leu	Phe	Tyr	Phe	Asn	Phe	Phe	Val	Tyr	Ala								
	435						440						445										
Ile	His	Ile	Ser	Ile	Leu	Thr	Thr	Ala	Ala	Tyr	Tyr	Arg	Pro	Val	Gln								
	450						455						460										
Lys	Gly	Asp	Lys	Pro	Pro	Phe	Ala	Phe	Gly	His	Ser	Thr	Gly	Glu	Tyr								
465						470						475						480					
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		485						490						495									
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	500						505						510										
Thr	Leu	Ile	Val	Asp	Ser	Tyr	Ser	Glu	Val	Leu	Phe	Phe	Val	His	Ser								
	515						520						525										
Leu	Leu	Leu	Leu	Ser	Ser	Val	Val	Leu	Tyr	Phe	Cys	Gly	Gln	Glu	Leu								
	530						535						540										
Tyr	Val	Ala	Ser	Met	Val	Phe	Ser	Leu	Ala	Leu	Gly	Trp	Ala	Asn	Met								
545						550						555						560					
Leu	Tyr	Tyr	Thr	Arg	Gly	Phe	Gln	Gln	Met	Gly	Ile	Tyr	Ser	Val	Met								
		565						570						575									
Ile	Ala	Lys	Met	Ile	Leu	Arg	Asp	Leu	Cys	Arg	Phe	Met	Phe	Val	Tyr								
	580						585						590										
Leu	Val	Phe	Leu	Leu	Gly	Phe	Ser	Thr	Ala	Val	Val	Thr	Leu	Ile	Glu								
	595						600						605										
Asp	Asp	Asn	Glu	Gly	Gln	Asp	Thr	Asn	Ser	Ser	Glu	Tyr	Ala	Arg	Cys								
	610						615						620										
Ser	His	Thr	Lys	Arg	Gly	Arg	Thr	Ser	Tyr	Asn	Ser	Leu	Tyr	Tyr	Thr								
625						630						635						640					
Cys	Leu	Glu	Leu	Phe	Lys	Phe	Thr	Ile	Gly	Met	Gly	Asp	Leu	Glu	Phe								
		645						650						655									
Thr	Glu	Asn	Tyr	Arg	Phe	Lys	Ser	Val	Phe	Val	Ile	Leu	Leu	Val	Leu								
	660						665						670										
Tyr	Val	Ile	Leu	Thr	Tyr	Ile	Leu	Leu	Leu	Asn	Met	Leu	Ile	Ala	Leu								
	675						680						685										
Met	Gly	Glu	Thr	Val	Ser	Lys	Ile	Ala	Gln	Glu	Ser	Lys	Ser	Ile	Trp								
	690						695						700										
Lys	Leu	Gln	Arg	Pro	Ile	Thr	Ile	Leu	Asp	Ile	Glu	Asn	Ser	Tyr	Leu								
705						710						715						720					
Asn	Cys	Leu	Arg	Arg	Ser	Phe	Arg	Ser	Gly	Lys	Arg	Val	Leu	Val	Gly								
		725						730						735									

05970303.04
F0570303.04

Ile	Thr	Pro	Asp	Gly	Gln	Asp	Asp	Tyr	Arg	Trp	Cys	Phe	Arg	Val	Asp
			740					745					750		
Glu	Val	Asn	Trp	Ser	Thr	Trp	Asn	Thr	Asn	Leu	Gly	Ile	Ile	Asn	Glu
		755					760					765			
Asp	Pro	Gly	Cys	Ser	Gly	Asp	Leu	Lys	Arg	Asn	Pro	Ser	Tyr	Cys	Ile
	770					775					780				
Lys	Pro	Gly	Arg	Val	Ser	Gly	Lys	Asn	Trp	Lys	Thr	Leu	Val	Pro	Leu
785					790					795					800
Leu	Arg	Asp	Gly	Ser	Arg	Arg	Glu	Glu	Thr	Pro	Lys	Leu	Pro	Glu	Glu
			805						810					815	
Ile	Lys	Leu	Lys	Pro	Ile	Leu	Glu	Pro	Tyr	Tyr	Glu	Pro	Glu	Asp	Cys
		820						825					830		
Glu	Thr	Leu	Lys	Glu	Ser	Leu	Pro	Lys	Ser	Val					
		835					840								

<210> 26

<211> 135

<212> DNA

<213> Homo sapiens

<400> 26

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<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> consensus

<400> 27

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<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> consensus

<400> 28

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<211> 135

<212> DNA

<213> chicken

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 <212> DNA
 <213> chicken

<400> 30
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 cttatagccc taatg 135

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 <212> DNA
 <213> Homo sapiens

<400> 31
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<210> 32
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 <212> DNA
 <213> Homo sapiens

<400> 32
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<210> 33
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 <212> DNA
 <213> Homo sapiens

<400> 33
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 caagccccag ctctccacgg ccaagagccg caccggctc tttgggaagg gtgactcgga 180
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<210> 34
<211> 839
<212> PRT
<213> Homo sapiens

<400> 34
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35 40 45
Leu Phe Gly Lys Gly Asp Ser Glu Glu Ala Phe Pro Val Asp Cys Pro
50 55 60
His Glu Glu Gly Glu Leu Asp Ser Cys Pro Thr Ile Thr Val Ser Pro
65 70 75 80
Val Ile Thr Ile Gln Arg Pro Gly Asp Gly Pro Thr Gly Ala Arg Leu
85 90 95
Leu Ser Gln Asp Ser Val Ala Ala Ser Thr Glu Lys Thr Leu Arg Leu
100 105 110
Tyr Asp Arg Arg Ser Ile Phe Glu Ala Val Ala Gln Asn Asn Cys Gln

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	130						135				140					
Thr	Asp	Asn	Glu	Phe	Lys	Asp	Pro	Glu	Thr	Gly	Lys	Thr	Cys	Leu	Leu	
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Lys	Ala	Met	Leu	Asn	Leu	His	Asp	Gly	Gln	Asn	Thr	Thr	Ile	Pro	Leu	
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Leu	Leu	Glu	Ile	Ala	Arg	Gln	Thr	Asp	Ser	Leu	Lys	Glu	Leu	Val	Asn	
			180					185					190			
Ala	Ser	Tyr	Thr	Asp	Ser	Tyr	Tyr	Lys	Gly	Gln	Thr	Ala	Leu	His	Ile	
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Phe	Val	Thr	Ser	Met	Tyr	Asn	Glu	Ile	Leu	Ile	Leu	Gly	Ala	Lys	Leu	
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His	Pro	Thr	Leu	Lys	Leu	Glu	Glu	Leu	Thr	Asn	Lys	Lys	Gly	Met	Thr	
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Ile	Leu	Gln	Arg	Glu	Ile	Gln	Glu	Pro	Glu	Cys	Arg	His	Leu	Ser	Arg	
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Lys	Phe	Thr	Glu	Trp	Ala	Tyr	Gly	Pro	Val	His	Ser	Ser	Leu	Tyr	Asp	
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Ala	Tyr	Ser	Ser	Ser	Glu	Thr	Pro	Asn	Arg	His	Asp	Met	Leu	Leu	Val	
				405				410					415			
Glu	Pro	Leu	Asn	Arg	Leu	Leu	Gln	Asp	Lys	Trp	Asp	Arg	Phe	Val	Lys	
			420					425				430				
Arg	Ile	Phe	Tyr	Phe	Asn	Phe	Leu	Val	Tyr	Cys	Leu	Tyr	Met	Ile	Ile	
	435					440					445					
Phe	Thr	Met	Ala	Ala	Tyr	Tyr	Arg	Pro	Val	Asp	Gly	Leu	Pro	Pro	Phe	
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[illegible]

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<211> 2380

<212> DNA

<213> Homo sapiens

<400> 35

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gggtgcctc	ccatggagtc	acagttccag	ggcgaggacc	ggaaattcgc	ccctcagata	180
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<210> 36
 <211> 764
 <212> PRT
 <213> Homo sapiens

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      20             25            30
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      35             40            45
Lys Phe Ala Pro Gln Ile Arg Val Asn Leu Asn Tyr Arg Lys Gly Thr
      50             55            60

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Gly 65	Ala	Ser	Gln	Pro	Asp	Pro	Asn	Arg	Phe	Asp	Arg	Asp	Arg	Leu	Phe
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Tyr	Leu	Ser	Lys	Thr	Ser	Lys	Tyr	Leu	Thr	Asp	Ser	Glu	Tyr	Thr	Glu
Gly	Ser	Thr	Gly	Lys	Thr	Cys	Leu	Met	Lys	Ala	Val	Leu	Asn	Leu	Lys
Asp	Gly	Val	Asn	Ala	Cys	Ile	Leu	Pro	Leu	Leu	Gln	Ile	Asp	Arg	Asp
Ser	Gly	Asn	Pro	Gln	Pro	Leu	Val	Asn	Ala	Gln	Cys	Thr	Asp	Asp	Tyr
Tyr	Arg	Gly	His	Ser	Ala	Leu	His	Ile	Ala	Ile	Glu	Lys	Arg	Ser	Leu
Gln	Cys	Val	Lys	Leu	Leu	Val	Glu	Asn	Gly	Ala	Asn	Val	His	Ala	Arg
Ala	Cys	Gly	Arg	Phe	Phe	Gln	Lys	Gly	Gln	Gly	Thr	Cys	Phe	Tyr	Phe
Gly	Glu	Leu	Pro	Leu	Ser	Leu	Ala	Ala	Cys	Thr	Lys	Gln	Trp	Asp	Val
Val	Ser	Tyr	Leu	Leu	Glu	Asn	Pro	His	Gln	Pro	Ala	Ser	Leu	Gln	Ala
Thr	Asp	Ser	Gln	Gly	Asn	Thr	Val	Leu	His	Ala	Leu	Val	Met	Ile	Ser
Asp	Asn	Ser	Ala	Glu	Asn	Ile	Ala	Leu	Val	Thr	Ser	Met	Tyr	Asp	Gly
Leu	Leu	Gln	Ala	Gly	Ala	Arg	Leu	Cys	Pro	Thr	Val	Gln	Leu	Glu	Asp
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Gly	Lys	Ile	Glu	Ile	Phe	Arg	His	Ile	Leu	Gln	Arg	Glu	Phe	Ser	Gly
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Arg	Val	Ser	Leu	Tyr	Asp	Leu	Ala	Ser	Val	Asp	Ser	Cys	Glu	Glu	Asn
Ser	Val	Leu	Glu	Ile	Ile	Ala	Phe	His	Cys	Lys	Ser	Pro	His	Arg	His
Arg	Met	Val	Val	Leu	Glu	Pro	Leu	Asn	Lys	Leu	Leu	Gln	Ala	Lys	Trp
Asp	Leu	Leu	Ile	Pro	Lys	Phe	Phe	Leu	Asn	Phe	Leu	Cys	Asn	Leu	Ile
Tyr	Met	Phe	Ile	Phe	Thr	Ala	Val	Ala	Tyr	His	Gln	Pro	Thr	Leu	Lys
Lys	Gln	Ala	Ala	Pro	His	Leu	Lys	Ala	Glu	Val	Gly	Asn	Ser	Met	Leu
Leu	Thr	Gly	His	Ile	Leu	Ile	Leu	Leu	Gly	Gly	Ile	Tyr	Leu	Leu	Val
Gly	Gln	Leu	Trp	Tyr	Phe	Trp	Arg	Arg	His	Val	Phe	Ile	Trp	Ile	Ser
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657030341054

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Pro Leu Leu Val Ser Ala Leu Val Leu Gly Trp Leu Asn Leu Leu Tyr						
	500		505		510	
Tyr Thr Arg Gly Phe Gln His Thr Gly Ile Tyr Ser Val Met Ile Gln						
	515		520		525	
Lys Val Ile Leu Arg Asp Leu Leu Arg Phe Leu Leu Ile Tyr Leu Val						
	530		535		540	
Phe Leu Phe Gly Phe Ala Val Ala Leu Val Ser Leu Ser Gln Glu Ala						
545		550		555		560
Trp Arg Pro Glu Ala Pro Thr Gly Pro Asn Ala Thr Glu Ser Val Gln						
	565		570		575	
Pro Met Glu Gly Gln Glu Asp Glu Gly Asn Gly Ala Gln Tyr Arg Gly						
	580		585		590	
Ile Leu Glu Ala Ser Leu Glu Leu Phe Lys Phe Thr Ile Gly Met Gly						
	595		600		605	
Glu Leu Ala Phe Gln Glu Gln Leu His Phe Arg Gly Met Val Leu Leu						
	610		615		620	
Leu Leu Leu Ala Tyr Val Leu Leu Thr Tyr Ile Leu Leu Leu Asn Met						
625		630		635		640
Leu Ile Ala Leu Met Ser Glu Thr Val Asn Ser Val Ala Thr Asp Ser						
	645		650		655	
Trp Ser Ile Trp Lys Leu Gln Lys Ala Ile Ser Val Leu Glu Met Glu						
	660		665		670	
Asn Gly Tyr Trp Trp Cys Arg Lys Lys Gln Arg Ala Gly Val Met Leu						
	675		680		685	
Thr Val Gly Thr Lys Pro Asp Gly Ser Pro Asp Glu Arg Trp Cys Phe						
	690		695		700	
Arg Val Glu Glu Val Asn Trp Ala Ser Trp Glu Gln Thr Leu Pro Thr						
705		710		715		720
Leu Cys Glu Asp Pro Ser Gly Ala Gly Val Pro Arg Thr Leu Glu Asn						
	725		730		735	
Pro Val Leu Ala Ser Pro Pro Lys Glu Asp Glu Asp Gly Ala Ser Glu						
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<210> 37
 <211> 21
 <212> DNA
 <213> Homo sapiens

<400> 37
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21

<210> 38
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[illegible]

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				20					25					30	
Pro	Pro	Pro	Val	Lys	Pro	His	Ile	Phe	Thr	Thr	Arg	Ser	Arg	Thr	Arg
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Leu	Phe	Gly	Lys	Gly	Asp	Ser	Glu	Glu	Ala	Ser	Pro	Leu	Asp	Cys	Pro
				50				55						60	
Tyr	Glu	Glu	Gly	Gly	Leu	Ala	Ser	Cys	Pro	Ile	Thr	Val	Ser	Ser	
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